

# Mahmoud Ahmed

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## SUMMARY

I use public high-throughput data to learn about the process of autophagy. I build open source tools for managing data in my lab, mainly R packages, and shiny applications.

## Education

Gyeongsang National University  
Graduate school  
Master of Science  
Grad. Feb. 2018

Cairo University  
Kasr-Alainy School of Medicine  
Bachelor of Medicine and Surgery  
Grad. May 2014

## Skills

Workflows: Genomic data processing,  
Network analysis  
Programming: R, Python  
Tools: docker, Git, LaTeX  
Languages: Arabic (native), English

## Certificates

Coursera Specializations: Mastering  
Software Development in R, Genomic  
Data Science, Data Science, Academic  
English: Writing  
edX Programs: Data Analysis for the  
Life Sciences, Genomics Data Analysis

## Volunteering

Staff member and outdoors activity instructor for youth and scout activity centers.  
Gilwell Park London, UK  
SAPSC Suncheon, SK  
Camp Lakota Ohio, USA

## RESEARCH

Gyeongsang National University 2016 – present  
Graduate Student Jinju, South Korea

- Investigating the role of the autophagy process in the development and differentiation of fat cells using public data.
- Building tools for managing and analyzing data.

## PUBLICATIONS

- Mahmoud Ahmed et al. “Transcriptional Regulation of Autophagy Genes via Stage-Specific Activation of CEBPB and PPARG during Adipogenesis: A Systematic Study Using Public Gene Expression and Transcription Factor Binding Datasets”. In: *Cells* 8.11 (Oct. 2019), p. 1321. ISSN: 2073-4409
- Mahmoud Ahmed et al. “Co-Expression network analysis of AMPK and autophagy gene products during adipocyte differentiation”. In: *International Journal of Molecular Sciences* 19.6 (June 2018), p. 1808. ISSN: 14220067
- Mahmoud Ahmed et al. “Functional Linkage of RKIP to the Epithelial to Mesenchymal Transition and Autophagy during the Development of Prostate Cancer”. In: *Cancers* 10.8 (Aug. 2018), p. 273. ISSN: 2072-6694

## OPEN SOURCE

- **colocr, R package** An R package for conducting co-localization analysis in fluorescence microscopy images.
- **cRegulome, R package** An R package to access, manage and visualize regulome (microRNA/transcription factors)-gene correlations in cancer.
- **pcr, R package** Quality assessing, analyzing and testing the statistical significance of real-time quantitative PCR data.
- **miRCancerdb, shiny web application** A database for microRNA-gene/protein expression correlation in cancer.

## TASK PREFERENCE

- ☆☆☆ Writing code to get and clean data
- ☆☆☆ Performing and reproducing an analysis
- ☆☆☆ Visualizing and presenting findings
- ☆☆☆ Writing a manuscript to be reviewed by strangers
- ☆☆☆ Arguing with the strangers